contained in the computer readable disk is identical to that of the paper copy. This amendment contains no new matter. Applicant submits that this amendment, the accompanying computer readable sequence listing, and the paper copy thereof serve to place this application in a condition of adherence to the rules 37 C.F.R. § 1.821-1.825.

Please direct any calls in connection with this application to the undersigned at (415) 781-1989.

Respectfully submitted,

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Dated: Dec. 14, 2001

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

Paragraph beginning at page 4, line 23, has been amended as follows:

– Figures 1A and 1B depict the germline ϵ locus and sequence. Fig. 1A depicts the sequence of the human IL-4 inducible ϵ promoter (SEQ ID NO:1). Fig. 1B depicts the organization of the germline ϵ locus.–

Paragraph beginning at page 4, line 27, has been amended as follows:

– Figures 2A and 2B depict the regions (2A) and sequences (2B and 2C; SEQ ID NOS:2&3) of the switch ϵ (Sϵ) region that are used in methods of screening for proteins that interact with the Sϵ region, as described below.–

Paragraph beginning at page 6, line 20, has been amended as follows:

– Figures 11A, 11B and 11C (SEQ ID NOS:4-6) depict preferred vectors and their sequences.–

Paragraph beginning at page 6, line 22, has been amended as follows:

– Figures 12A, 12B and 12C (SEQ ID NO:7) depict a construct useful in the present invention, comprising the a Fas survival construct (i.e. the use of a death gene). The sequence is of the inducible ϵ promoter-chimeric Fas-IRES-hygromycin-bovine growth hormone poly A tail that is put into the C12s vector backwards to that no leaky transcription happens through the cmv promoter.–

Paragraph beginning at page 6, line 27, has been amended as follows:

– Figures 13A, 13B and 13C (SEQ ID NO:8) depict a construct useful in the present invention, comprising the a Fas survival construct (i.e. the use of a death gene). The sequence is of the inducible ϵ promoter-chimeric Fas (either CD8 or mLyt2)-IRES-hygromycin-bovine growth hormone poly A tail that is put into the C12s vector backwards to that no leaky transcription happens through the cmv promoter.–

Paragraph beginning at page 28, line 14, has been amended as follows:

– A preferred coiled-coil presentation structure is as follows:

MGCAALESEVSALESEVASLESEVAAL**GRGDMP**LAAVKSKLSAVKSKLASVKS KLAACGPP (SEQ ID NO:9). The underlined regions represent a coiled-coil leucine zipper region defined previously (see Martin et al., EMBO J. 13(22):5303-5309 (1994), incorporated by reference). The bolded GRGDMP (SEQ ID NO:10) region represents the loop structure and when appropriately replaced with randomized peptides (i.e.candidate bioactive agents, generally depicted herein as $(X)_n$, where X is an amino acid residue and n is an integer of at least 5 or 6) can be of variable length. The replacement of the bolded region is facilitated by encoding restriction endonuclease sites in the underlined regions, which allows the direct incorporation of randomized oligonucleotides at these positions. For example, a preferred embodiment generates a XhoI site at the double underlined LE site and a HindIII site at the double-underlined KL site.–

Paragraph beginning at page 29, line 6, has been amended as follows:

– A preferred minibody presentation structure is as follows:

MGRNSQATS**GFT*F*SHF**YMEWVRGGEYIAASR**HKHNKY**TTEYSASVKGRYIVSR DTSQSILYLQKKKGPP (SEQ ID NO:11). The bold, underline regions are the regions which may be randomized. The ~~italized~~ italicized phenylalanine must be invariant in the first randomizing region. The entire peptide is cloned in a three-oligonucleotide variation of the coiled-coil embodiment, thus allowing two different randomizing regions to be incorporated simultaneously. This embodiment utilizes non-palindromic BstXI sites on the termini.–

Paragraph beginning at page 30, line 6, has been amended as follows:

– In a preferred embodiment, the targeting sequence is a nuclear localization signal (NLS). NLSs are generally short, positively charged (basic) domains that serve to direct the entire protein in which they occur to the cell's nucleus. Numerous NLS amino acid sequences have been reported including single basic ~~NLS's~~ NLSs such as that of the SV40 (monkey virus) large T Antigen (Pro Lys Lys Lys Arg Lys Val (SEQ ID NO:12)), Kalderon (1984), et al., Cell, 39:499-509; the human retinoic acid receptor-ß nuclear localization signal (ARRRRP (SEQ ID NO:13)); NFκB p50 (EEVQRKRQKL (SEQ ID NO:14); Ghosh et al., Cell 62:1019 (1990); NFκB p65 (EEKRKRTYE (SEQ ID NO:15); Nolan et al., Cell 64:961 (1991); and others (see for example Boulikas, J. Cell. Biochem. 55(1):32-58 (1994), hereby incorporated by reference) and double basic ~~NLS's~~ NLSs exemplified by that of the Xenopus (African clawed toad) protein, nucleoplasmin (Ala

Val Lys Arg Pro Ala Ala Thr Lys Lys Ala Gly Gln Ala Lys Lys Lys Lys Leu Asp (SEQ ID NO:16)), Dingwall, et al., Cell, 30:449-458, 1982 and Dingwall, et al., J. Cell Biol., 107:641-849; 1988). Numerous localization studies have demonstrated that NLSs incorporated in synthetic peptides or grafted onto reporter proteins not normally targeted to the cell nucleus cause these peptides and reporter proteins to be concentrated in the nucleus. See, for example, Dingwall, and Laskey, Ann, Rev. Cell Biol., 2:367-390, 1986; Bonnerot, et al., Proc. Natl. Acad. Sci. USA, 84:6795-6799, 1987; Galileo, et al., Proc. Natl. Acad. Sci. USA, 87:458-462, 1990.–

Paragraph beginning at page 31, line 5, has been amended as follows:

– In a preferred embodiment, the fusion partner is a stability sequence to confer stability to the candidate bioactive agent or the nucleic acid encoding it. Thus, for example, peptides may be stabilized by the incorporation of glycines after the initiation methionine (MG or MGG0), for protection of the peptide to ubiquitination as per Varshavsky's N-End Rule, thus conferring long half-life in the cytoplasm. Similarly, two prolines at the C-terminus impart peptides that are largely resistant to carboxypeptidase action. The presence of two glycines prior to the prolines impart both flexibility and prevent structure initiating events in the di-proline to be propagated into the candidate peptide structure. Thus, preferred stability sequences are as follows: $MG(X)_nGGPP$ (SEQ ID NO:17), where X is any amino acid and n is an integer of at least four.–

Paragraph beginning at page 32, line 28, has been amended as follows:

– In a preferred embodiment, the fusion partner includes a linker or tethering sequence, as generally described in PCT US 97/01019, that can allow the candidate agents to interact with potential targets unhindered. For example, when the candidate bioactive agent is a peptide, useful linkers include glycine-serine polymers (including, for example, $(GS)_n$, $(GSGGS)_n$ (SEQ ID NO:18) and $(GGGS)_n$ (SEQ ID NO:19), where n is an integer of at least one), glycine-alanine polymers, alanine-serine polymers, and other flexible linkers such as the tether for the shaker potassium channel, and a large variety of other flexible linkers, as will be appreciated by those in the art. Glycine-serine polymers are preferred since both of these amino acids are relatively unstructured, and therefore may be able to serve as a neutral tether between components. Secondly, serine is hydrophilic and therefore able to solubilize what could be a globular glycine chain. Third, similar chains have been shown to be effective in joining subunits of recombinant proteins such as single chain antibodies.–

On page 59, immediately preceding the heading "CLAIMS," the enclosed text entitled "Sequence Listing" was inserted into the specification.

IN THE CLAIMS:

Claim 28 has been amended as follows:

– 2. (Amended) A method of identifying proteins that bind to all or part of the switch ϵ region of Figure 2B (SEQ ID NO:2), said method comprising:

a) providing a host cell comprising the composition of claim 27;

b) subjecting said host cell to conditions under which the fusion gene is expressed to produce a fusion protein; and

c) determining whether a protein-nucleic acid interaction between said fusion protein and said switch ϵ sequence occurred.